



1600

## RAW SEQUENCE LISTING

DATE: 08/01/2003

PATENT APPLICATION: US/09/973,382B

TIME: 14:40:52

Input Set : N:\Crf4\07302003\I973282B.raw

Output Set: N:\CRF4\08012003\I973382B.raw

1 <110> APPLICANT: Heston, Warren D.W.  
 2 O'Keefe, Denise S.  
 3 <120> TITLE OF INVENTION: DNA Encoding the Prostate-Specific Membrane  
 4 Antigen-Like Gene and Uses Thereof  
 5 <130> FILE REFERENCE: D6230  
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/973,382B  
 7 <141> CURRENT FILING DATE: 2001-10-09  
 8 <150> PRIOR APPLICATION NUMBER: PCT/US00/09417  
 9 <151> PRIOR FILING DATE: 2000-04-09  
 10 <160> NUMBER OF SEQ ID NOS: 38  
 12 <210> SEQ ID NO: 1  
 13 <211> LENGTH: 1992  
 14 <212> TYPE: DNA  
 15 <213> ORGANISM: Homo sapiens  
 16 <220> FEATURE:  
 17 <223> OTHER INFORMATION: cDNA sequence of PSMA-like gene  
 18 <400> SEQUENCE: 1  
 19 agcaaatact cactaccaca aataagaaca ttccaaatc tgatgttctg 50  
 20 aggattttta gagcttatag tagcaaaaag aaaagggaaa ttctctctga 100  
 21 gatgtccttt tttgtaggcc taatgacaaa aggttgaaga taaagtctta 150  
 22 gtactcattt aagtgttaata ttgaaaattg atattaccaa atctggaaca 200  
 23 accaatttta aataaggaaa gaaagacact gtgttttcta ggttaaaaat 250  
 24 gccagctggg caggggccaa aggagtcatt ctctactcag accctgctga 300  
 25 ctactttgct cctgggggtga agtcttatcc agacgggttg aatcttcctg 350  
 26 gaggtgggtg ccagcgtgga aatatacctaa atctgaatgg tgcaggagac 400  
 27 cctctcacac caggttaccc agcaaatgaa tacgcttata ggcatggaat 450  
 28 tgcagaggct gttggtcttc caagtattcc tgttcatcca gttggatact 500  
 29 atgatgcaca gaagctccta gaaaaaatgg gtggctcagc accaccagat 550  
 30 agcagctgga gaggaagtct caaagtgtcc tacaatgttg gacctggctt 600  
 31 tactggaaac ttttctacac aaaaagtcaa gatgcacac cactctacca 650  
 32 atgaagtgcac gagaatttac aatgtgatag gtactctcag aggagcagtg 700  
 33 gaaccagaca gatatgtcat tctgggaggt caccgggact catgggtggt 750  
 34 tgggtggtatt gaccctcaga gtggagcagc tgttggtcat gaaactgtga 800  
 35 ggagcttttg aacactgaaa aaggaagggt ggagacctag aagaacaatt 850  
 36 ttgtttgcaa gctgggatgc agaagaattt ggtcttcttg gttctactga 900  
 37 gtgggcagag gataattcaa gactccttca agagcgtggc gtggcttata 950  
 38 ttaatgctga ctcatctata gaaggaaact acactctgag agttgattgt 1000  
 39 acaccactga tgtacagctt ggtatacaac ctaacaaaag agctgaaaag 1050  
 40 ccctgatgaa ggctttgaag gcaaatctct ttatgaaagt tggactaaaa 1100  
 41 aaagtccttc ccagaggttc agtggcatgc ccaggataag caaattggga 1150  
 42 tctggaaatg attttgaggt gttcttccaa cgacttgga ttgcttcagg 1200  
 43 cagagcacgg tatactaaaa attgggaaac aaacaaattc agcggctatc 1250  
 44 cactgtatca cagtgtctat gaaacatatg agttgggtga aaagttttat 1300

Does Not Comply  
Corrected Diskette Needed

7.3

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45      gatccaatgt ttaaatatca cctcactgtg gccaggttc gaggaggat 1350
46      ggtgtttgag ctagccaatt ccatagtgtc cccttttgat tgctgagatt 1400
47      atgctgtagt tttaagaaag tatgctgaca aaatctacaa tatttctatg 1450
48      aaacatccac aggaaatgaa gacatacagt ttatcatttg attcactttt 1500
49      ttctgcagta aaaaatttta cagaaattgc ttccaagttc agcgagagac 1550
50      tccaggactt tgacaaaagc aacccaatat tgttaagaat gatgaatgat 1600
51      caactcatgt ttctggaaag agcatttatt gatccattag ggttaccaga 1650
52      cagacctttt tataggcatg tcatctatgc tccaagcagc cacaacaagt 1700
53      atgcagggga gtcattccca ggaatttatg atgctctgtt tgatattgaa 1750
54      agcaaagtgg acccttccaa ggctgggga gatgtgaaga gacagatttc 1800
55      tggtgcagcc ttcacagtgc aggcagctgc agagactttg agtgaagtag 1850
56      cctaagagga ttcttttagag actctgtatt gaatttgtgt ggtatgtcac 1900
57      tcaaagaata ataatgggta tattgataaa ttttaaaatt ggtatatttg 1950
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60 &lt;210&gt; SEQ ID NO: 2

61 &lt;211&gt; LENGTH: 442

62 &lt;212&gt; TYPE: PRT

63 &lt;213&gt; ORGANISM: Homo sapiens

64 &lt;220&gt; FEATURE:

65 &lt;223&gt; OTHER INFORMATION: deduced amino acid sequence of PSMA-like protein

67 &lt;400&gt; SEQUENCE: 2

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68      Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg Gly Ser Leu
69              5                      10                      15
70      Lys Val Ser Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn Phe Ser
71              20                      25                      30
72      Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val Thr
73              35                      40                      45
74      Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
75              50                      55                      60
76      Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe
77              65                      70                      75
78      Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Thr
79              80                      85                      90
80      Val Arg Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg
81              95                      100                     105
82      Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu
83              110                     115                     120
84      Leu Gly Ser Thr Glu Trp Ala Glu Asp Asn Ser Arg Leu Leu Gln
85              125                     130                     135
86      Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly
87              140                     145                     150
88      Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu
89              155                     160                     165
90      Val Tyr Asn Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe
91              170                     175                     180
92      Glu Gly Lys Ser Leu Tyr Glu Ser Trp Thr Lys Lys Ser Pro Ser
93              185                     190                     195
94      Pro Glu Phe Ser Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly

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95          200          205          210
96  Asn Asp Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly
97          215          220          225
98  Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn Lys Phe Ser Gly
99          230          235          240
100  Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu Leu Val Glu
101          245          250          255
102  Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val Ala Gln
103          260          265          270
104  Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val Leu
105          275          280          285
106  Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
107          290          295          300
108  Asp Lys Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met Lys
109          305          310          315
110  Thr Tyr Ser Leu Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn
111          320          325          330
112  Phe Thr Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe
113          335          340          345
114  Asp Lys Ser Asn Pro Ile Leu Leu Arg Met Met Asn Asp Gln Leu
115          350          355          360
116  Met Phe Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp
117          365          370          375
118  Arg Pro Phe Tyr Arg His Val Ile Tyr Ala Pro Ser Ser His Asn
119          380          385          390
120  Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe
121          395          400          405
122  Asp Ile Glu Ser Lys Val Asp Pro Ser Lys Ala Trp Gly Asp Val
123          410          415          420
124  Lys Arg Gln Ile Ser Val Ala Ala Phe Thr Val Gln Ala Ala Ala
125          425          430          435
126  Glu Thr Leu Ser Glu Val Ala
127          440

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129 &lt;210&gt; SEQ ID NO: 3

130 &lt;211&gt; LENGTH: 2653

131 &lt;212&gt; TYPE: DNA

132 &lt;213&gt; ORGANISM: Homo sapiens

133 &lt;220&gt; FEATURE:

134 &lt;223&gt; OTHER INFORMATION: nucleotide sequence of human PSMA gene

135 &lt;300&gt; PUBLICATION INFORMATION:

136 &lt;308&gt; DATABASE ACCESSION NO: GenBank Accession No. M99487

W--&gt; 137 &lt;309&gt; DATABASE ENTRY DATE:

W--&gt; 138 &lt;300&gt; PUBLICATION INFORMATION: 3

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139  ctcaaaagg ggcggatttc cttctcctgg aggcagatgt tgcctctctc 50
140  tctcgctcgg attggttcag tgcactctag aaacactgct gtggtggaga 100
141  aactggaccc caggtctgga gcgaattcca gcctgcaggg ctgataagcg 150
142  aggcattagt gagattgaga gagactttac cccgccgtgg tggttggagg 200
143  gcgcgcagta gagcagcagc acagggcgcg gtcccgggag gccggtctct 250
144  ctcgcgccga gatgtggaat ctccttcacg aaaccgactc ggctgtggcc 300

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mandatory response needed  
whenever <308> has a response.

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145 accgcgcgcc gccgcgcgtg gctgtgcgct ggggcgcgtg tgctggcggg 350
146 tggcttcttt ctctctgggt tctctcttgg gtggtttata aaatcctcca 400
147 atgaagctac taacattact ccaaagcata atatgaaagc atttttggat 450
148 gaattgaaaag ctgagaacat caagaagttc ttatataatt ttacacagat 500
149 accacattta gcaggaacag aacaaaactt tcagcttgca aagcaaattc 550
150 aatcccagtg gaaagaattt ggccctggatt ctgttgagct agcacattat 600
151 gatgtcctgt tgtcctaccc aaataagaact catcccaact acatctcaat 650
152 aattaatgaa gatggaaatg agattttcaa cacatcatta tttgaaccac 700
153 ctctccagg atatgaaaat gtttcggata ttgtaccacc tttcagtgtc 750
154 ttctctctc aaggaatgcc agagggcgat ctagtgtatg ttaactatgc 800
155 acgaactgaa gacttcttta aattggaacg ggacatgaaa atcaattgct 850
156 ctgggaaaat tgtaattgcc agatatggga aagttttcag aggaaataag 900
157 gttaaaaatg ccagctggc aggggccaag ggagtcattc tctactccga 950
158 ccctgctgac tactttgtct ctggggtgaa gtccctatcca gatggttga 1000
159 atcttcttgg aggtggtgtc cagcgtggaa atatcctaaa tctgaatggt 1050
160 gcaggagacc ctctcacacc aggttaccca gcaaatgaat atgcttatag 1100
161 gcgtggaatt gcagaggtg ttggtcttcc aagtattcct gttcatccaa 1150
162 ttggatacta tgatgcacag aagctcctag aaaaaatggg tggctcagca 1200
163 ccaccagata gcagctggag aggaagtctc aaagtgcctt acaatgttgg 1250
164 acctggcttt actggaact tttctacaca aaaagtcaag atgcacatcc 1300
165 actctaccaa tgaagtgaca agaatttaca atgtgatagg tactctcaga 1350
166 ggagcagtg gacagacag atatgtcatt ctgggaggtc accgggactc 1400
167 atgggtgttt ggtggtattg accctcagag tggagcagct gttgttcatg 1450
168 aaattgtgag gagctttgga aactgaaaa aggaagggtg gagacctaga 1500
169 agaacaattt tgtttgcaag ctgggatgca gaagaatttg gtcttcttgg 1550
170 ttctactgag tgggcagagg agaattcaag actccttcaa gagcgtggcg 1600
171 tggcttatat taatgctgac tcacttatag aaggaaacta cactctgaga 1650
172 gttgattgta caccgctgat gtacagcttg gtacacaacc taacaaaaga 1700
173 gctgaaaagc cctgatgaag gctttgaagg caaatctctt tatgaaagtt 1750
174 ggactaaaaa aagtccttcc ccagagttca gtggcatgcc caggataagc 1800
175 aaattgggat ctggaaatga ttttgaggtg ttcttccaac gacttggat 1850
176 tgcttcaggc agagcacggt aactaaaaa ttgggaaaca aacaaattca 1900
177 gcggtatcc actgtatcac agtgtctatg aaacatatga gttggtggaa 1950
178 aagttttatg atccaatgtt taaatatcac ctactgttg cccaggttcg 2000
179 aggagggatg gtgtttgagc tagccaattc catagtgtc ccttttgatt 2050
180 gtcgagatta tgctgtagtt ttaagaaagt atgctgacaa aatctacagt 2100
181 atttctatga aacatccaca ggaaatgaag acatacagt tatcatttga 2150
182 ttcaactttt tctgcagtaa agaattttac agaaattgct tccaagttca 2200
183 gtgagagact ccaggacttt gacaaaagca acccaatagt attaagaatg 2250
184 atgaatgatc aactcatgtt tctggaaaga gcatttattg atccattagg 2300
185 gttaccagac aggccttttt ataggcatgt catctatgct ccaagcagcc 2350
186 acaacaagta tgcaggggag tcattcccag gaatttatga tgctctgttt 2400
187 gatattgaaa gcaaagtgga cccttccaag gcctggggag aagtgaagag 2450
188 acagatttat gttgcagcct tcacagtgc ggcagctgca gagactttga 2500
189 gtgaagtage ctaagaggat tctttagaga atccgtattg aatttggtgtg 2550
190 gtatgtcact cagaaagaat cgtaatgggt atattgataa attttaaaat 2600
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192 aaa 2653
194 <210> SEQ ID NO: 4

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195 <211> LENGTH: 750
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
198 <220> FEATURE:
199 <223> OTHER INFORMATION: deduced amino acid sequence of PSMA protein
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205 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
206           35                      40                      45
207 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
208           50                      55                      60
209 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr
210           65                      70                      75
211 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
212           80                      85                      90
213 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
214           95                      100                     105
215 Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro
216          110                     115                     120
217 Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly
218          125                     130                     135
219 Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly
220          140                     145                     150
221 Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
222          155                     160                     165
223 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala
224          170                     175                     180
225 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
226          185                     190                     195
227 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
228          200                     205                     210
229 Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val
230          215                     220                     225
231 Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
232          230                     235                     240
233 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg
234          245                     250                     255
235 Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro
236          260                     265                     270
237 Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu
238          275                     280                     285
239 Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr
240          290                     295                     300
241 Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro
242          305                     310                     315
243 Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly

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VERIFICATION SUMMARY

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Input Set : N:\Crf4\07302003\I973282B.raw

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L:6 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:137 M:286 W: Invalid Database Entry: Valid Formats YYYY-MM-DD or Mon-YYYY, SEQ ID:3  
L:138 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:3